

D. Fitzgerald

1646

#14

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,159A

DATE: 09/01/1999  
TIME: 15:15:13

INPUT SET: S33153.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Lee, Jong Y.  
6  
7 (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR  
8 PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM  
9  
10 (iii) NUMBER OF SEQUENCES: 5  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Fish & Richardson P.C., P.A.  
14 (B) STREET: 60 South Sixth Street, Suite 3300  
15 (C) CITY: Minneapolis  
16 (D) STATE: MN  
17 (E) COUNTRY: USA  
18 (F) ZIP: 55402  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Floppy disk  
22 (B) COMPUTER: IBM compatible  
23 (C) OPERATING SYSTEM: DOS  
24 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER: 09/016,159  
28 (B) FILING DATE: 30-JAN-1998  
29  
30 (vi) PRIOR APPLICATION DATA:  
31 (A) APPLICATION NUMBER: 08/876,227  
32 (B) FILING DATE: 16-JUN-1997  
33  
34 (vi) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: 08/734,097  
36 (B) FILING DATE: 21-OCT-1996  
37  
38 (vi) PRIOR APPLICATION DATA:  
39 (A) APPLICATION NUMBER: 08/460,525  
40 (B) FILING DATE: 02-JUN-1995  
41  
42 (viii) ATTORNEY/AGENT INFORMATION:  
43 (A) NAME: Ellinger, Mark S.  
44 (B) REGISTRATION NUMBER: 34,812  
45 (C) REFERENCE/DOCKET NUMBER: 07004/002004  
46

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,159ADATE: 09/01/1999  
TIME: 15:15:14

INPUT SET: S33153.raw

47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: 612/335-5070  
49 (B) TELEFAX: 612/288-9696  
50  
51  
52 (2) INFORMATION FOR SEQ ID NO:1:  
53  
54 (i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 23 base pairs  
56 (B) TYPE: nucleic acid  
57 (C) STRANDEDNESS: single  
58 (D) TOPOLOGY: linear  
59  
60 (ii) MOLECULE TYPE: synthetic DNA  
61  
62 (iii) HYPOTHETICAL: NO  
63  
64 (iv) ANTI-SENSE: NO  
65  
66  
67 (ix) FEATURE:  
68 (A) NAME/KEY: BamH1 linker ar 5' end followed by sequence for amino  
69 acids 25 through 29 of the full length human Epor protein. Forward primer for  
70 Sequence ID No. 2."  
71  
72  
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
74  
75 TTGGATCC GCG CCC CCG CCT A AC 23  
76 Ala Pro Pro Pro  
77 1  
78  
79 (2) INFORMATION FOR SEQ ID NO:2:  
80  
81 (i) SEQUENCE CHARACTERISTICS:  
82 (A) LENGTH: 22 base pairs  
83 (B) TYPE: nucleic acid  
84 (C) STRANDEDNESS: single  
85 (D) TOPOLOGY: linear  
86  
87 (ii) MOLECULE TYPE: synthetic DNA  
88  
89 (iii) HYPOTHETICAL: NO  
90  
91 (iv) ANTI-SENSE: NO  
92  
93  
94 (ix) FEATURE:  
95 (A) NAME/KEY: EcoR1 linker followed by sequence complementary to  
96 coding sequence for amino acids 226 through 222 of full length human Epor  
97 protein. Reverse primer for Sequence ID No. 1.  
98  
99

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/016,159ADATE: 09/01/1999  
TIME: 15:15:14

INPUT SET: S33153.raw

100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
101  
102 TGAATTCGGG GTCCAGGTCG CT 22  
103  
104 (2) INFORMATION FOR SEQ ID NO:3:  
105  
106 (i) SEQUENCE CHARACTERISTICS:  
107 (A) LENGTH: 18 base pairs  
108 (B) TYPE: nucleic acid  
109 (C) STRANDEDNESS: double  
110 (D) TOPOLOGY: linear  
111  
112 (ii) MOLECULE TYPE: other nucleic acid  
113  
114 (iii) HYPOTHETICAL: NO  
115  
116 (iv) ANTI-SENSE: NO  
117  
118 (vi) ORIGINAL SOURCE:  
119 (A) ORGANISM: Homo sapiens  
120  
121 (vii) IMMEDIATE SOURCE:  
122 (B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)  
123  
124 (ix) FEATURE:  
125 (A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."  
126  
127 (x) PUBLICATION INFORMATION:  
128 (A) AUTHORS: Smith, D.B.  
129 Johnson, K.S.  
130 (B) TITLE: Single-step purification of polypeptides  
131 expressed in Escherichia coli as fusions with  
132 glutathione-S-transferase  
133 (D) VOLUME: 67  
134 (F) PAGES: 31-40  
135 (G) DATE: 1988  
136  
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
138  
139 CTG GTT CCG CGT GGA T CC 18  
140 Leu Val Pro Arg Gly  
141 5  
142  
143 (2) INFORMATION FOR SEQ ID NO:4:  
144  
145 (i) SEQUENCE CHARACTERISTICS:  
146 (A) LENGTH: 1527 base pairs  
147 (B) TYPE: nucleic acid  
148 (C) STRANDEDNESS: double  
149 (D) TOPOLOGY: linear  
150  
151  
152 (x) PUBLICATION INFORMATION:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/016,159A

DATE: 09/01/1999  
TIME: 15:15:14

INPUT SET: S33153.raw

```

153      (A) AUTHORS: Winkelmann , J. C., et al.
154      (C) JOURNAL: Blood
155      (D) VOLUME: 76
156      (E) ISSUE: 1
157      (F) PAGES: 24-30
158      (G) DATE: 1990
159
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
161
162      ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT      48
163      Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
164      1          5          10          15
165
166      CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC      96
167      Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
168      20          25          30
169
170      CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA      144
171      Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
172      35          40          45
173
174      GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG      192
175      Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
176      50          55          60
177
178      GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC      240
179      Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
180      65          70          75          80
181
182      TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT      288
183      Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
184      85          90          95
185
186      CCC ACG GCT CGT GGT CGG GTG CGC TTC TGG TGT TCG CTG CCT ACA GCC      336
187      Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
188      100         105         110
189
190      GAC ACG TCG AGC TTC GTG CCC CTA GAG TTG CGC GTC ACA GCA GCC TCC      384
191      Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
192      115         120         125
193
194      GGC GCT CCG CGA TAT CAC CGT GTC ATC CAC ATC AAT GAA GTA GTG CTC      432
195      Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
196      130         135         140
197
198      CTA GAC GCC CCC GTG GGG CTG GTG GCG CGG TTG GCT GAC GAG AGC GGC      480
199      Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
200      145         150         155         160
201
202      CAC GTA GTG TTG CGC TGG CTC CCG CCG CCT GAG ACA CCC ATG ACG TCT      528
203      His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
204      165         170         175
205

```

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/016,159A

DATE: 09/01/1999  
TIME: 15:15:15

INPUT SET: S33153.raw

206	CAC ATC CGC TAC GAG GTG GAC GTC TCG GCC GGC AAC CGG CCA GGG AGC	576
207	His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser	
208	180 185 190	
209		
210	GTA CAG AGG GTG GAG ATC CTG GAG GGC CGC ACC GAG TGT GTG CTG AGC	624
211	Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser	
212	195 200 205	
213		
214	AAC CTG CGG GGC CGG ACG CGC TAC ACC TTC GCC GTC CGC GCG CGT ATG	672
215	Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met	
216	210 215 220	
217		
218	GCT GAG CCG AGC TTC GGC GGC TTC TGG AGC GCC TGG TCG GAG CCT GTG	720
219	Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val	
220	225 230 235 240	
221		
222	TCG CTG CTG GAG CCT AGC GAC CTG GAC CCC CTC ATC CTG ACG CTC TCC	768
223	Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser	
224	245 250 255	
225		
226	CTC ATC CTC GTG GTC ATC CTG GTG CTG CTG ACC GTG CTC GCG CTG CTC	816
227	Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu	
228	260 265 270	
229		
230	TCC CAC CGC CGG GCT CTG AAG CAG AAG ATC TGG CCT GGC ATC CCG AGC	864
231	Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser	
232	275 280 285	
233		
234	CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC	912
235	Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe	
236	290 295 300	
237		
238	CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC	960
239	Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys	
240	305 310 315 320	
241		
242	ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG	1008
243	Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu	
244	325 330 335	
245		
246	CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG	1056
247	Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu	
248	340 345 350	
249		
250	GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT	1104
251	Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr	
252	355 360 365	
253		
254	CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC	1152
255	Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp	
256	370 375 380	
257		
258	CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC	1200

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/016,159A**

DATE: 09/01/1999  
TIME: 15:15:15

***INPUT SET: S33153.raw***

Line

Error

Original Text